

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Original) A transformed plant, characterized in that it expresses at least one leghemoglobin.
2. (Previously presented) The transformed plant according to claim 1, characterized in that it comprises at least one sequence of SEQ ID NO: 1 coding for a leghemoglobin.
3. (Previously presented) The transformed plant according to claim 2, characterized in that it comprises a sequence which has approximately 70% identity with the sequence of SEQ ID NO: 1.
4. (Currently amended) ~~The~~ A transformed plant characterized in that it expresses at least one hemoglobin or at least one leghemoglobin and at least one Hemoglobin.
5. (Previously presented) The transformed plant according to claim 4, characterized in that the leghemoglobin and/or hemoglobin is selected from plants from the group consisting of *Lupinus luteus*, *Glycine max*, *Medicago sativa*, *Medicago trunculata*, *Phaseolus vulgaris*, *Vicia faba*, *Pisum sativum*, *Vigna unguiculata*, *Lotus japonicus*, *Psophocarpus tetragonolobus*, *Sesbania rostrata*, *Casuarina glauca* and *Canvalaria lineata*.
6. (Previously presented) The transformed plant according to claim 4, characterized in that the leghemoglobin and/or hemoglobin is derived from *Lotus japonicus* and *Arabidopsis thaliana*.
7. (Previously presented) The transformed plant according to claim 4, characterized in that it expresses the leghemoglobin and/or hemoglobin in a storage-organ-specific manner.
8. (Previously presented) The transformed plant according to claim 4, characterized in that it expresses the at least one leghemoglobin and/or hemoglobin in a tuber-specific and/or seed-specific manner.
9. (Previously presented) The transformed plant according to claim 4, characterized in that it comprises at least one of the sequences of SEQ ID NOS: 3 and 5 coding for hemoglobin or at

least one sequence of SEQ ID NO: 1 coding for a leghemoglobin and at least one of the sequences of SEQ ID NOS: 3 and 5 coding for hemoglobin.

10. (Previously presented) The transformed plant according to claim 4, characterized in that it comprises sequences with approximately 70% identify with the sequences of SEQ ID NOS: 1, 3 and/or 5.
11. (Previously presented) The transformed plant according to claim 4, characterized in that it produces starch and/or oil.
12. (Previously presented) The transformed plant according to claim 4, characterized in that it is a monocotyledonous crop plant, in particular of the species Gramineae.
13. (Previously presented) The transformed plant according to claim 4, characterized in that it is a dicotyledonous crop plant, in particular from the family, Asteraceae, Brassicaceae, Compositae, Cruciferae, Cucurbitaceae, Leguminosae, Rubiaceae, Solanaceae, Sterculiaceae, Theaceae or Umbelliferae.
14. (Original) The transformed plant according to claim 13, characterized in that it is potato, *Arabidopsis thaliana*, soybean or oilseed rape.
15. (Previously presented) A nucleotide sequence as shown in sequence of SEQ ID NO: 1, coding for leghemoglobin for use in a plant according to claim 4.
16. (Original) A gene structure comprising at least one nucleotide sequence according to claim 15.
17. (Previously presented) A vector comprising at least one or more nucleotide sequences according to claim 15.
18. (Previously presented) A transformed plant comprising at least one gene structure according to claim 16.

19. (Previously presented) A transformed plant comprising at least one vector according to claim 17.
20. (Previously presented) A nucleotide sequence as shown in the sequences of SEQ ID NOS: 3 and 5 coding for hemoglobin for use in a plant according to claim 4.
21. (Original) A gene structure comprising at least one nucleotide sequence according to claim 20.
22. (Previously presented) A vector comprising at least one or more nucleotide sequences according to claim 20.
23. (Previously presented) A transformed plant comprising at least one gene structure according to claim 21.
24. (Previously presented) A transformed plant comprising at least one gene structure according to claim 22.
25. (Original) A method for modifying the storage reserve content in plants, characterized in that it comprises transforming plants in such a way that they express at least one leghemoglobin.
26. (Previously presented) The method according to claim 25, characterized in that the plants are transformed in such a way that they comprise at least one sequence of SEQ ID NO: 1 coding for a leghemoglobin.
27. (Previously presented) The method according to claim 25, characterized in that plants are transformed in such a way that they comprise a sequence with approximately 70% identity with the sequence of SEQ ID NO: 1.
28. (Original) A method for modifying the storage reserve content in plants, characterized in that it comprises transforming plants in such a way that they express at least Hemoglobin or one leghemoglobin and at least one hemoglobin.

29. (Previously presented) The method according to claim 28, characterized in that the leghemoglobin and hemoglobin is selected from plants of the group consisting of *Arabidopsis thaliana*, *Lupinus luteus*, *Glycine max*, *Medicago sativa*, *Medicago trunculata*, *Phaseolus vulgaris*, *Vicia faba*, *Pisum sativum*, *Vigna unguiculata*, *Lotus japonicus*, *Psophocarpus tetragonolobus*, *Sesbania rostrata*, *Casuarina glauca* and *Canvalaria lineatea*.
30. (Previously presented) The method according to claim 28, characterized in that the leghemoglobin and/or hemoglobin is derived from *Lotus japonicus* and *Arabidopsis thaliana*.
31. (Previously presented) The method according to claim 28, characterized in that the plants are transformed in such a way that they express the leghemoglobin and Hemoglobin in a storage-organ-specific manner.
32. (Previously presented) The method according to claim 28, characterized in that the plants are transformed in such a way that they express the leghemoglobin and hemoglobin in a tuber-specific and/or seed-specific manner.
33. (Previously presented) The method according to claim 28, characterized in that the plants are transformed in such a way that they comprise at least one sequence of SEQ ID NOS: 3 and/or 5 coding for hemoglobin or at least one sequence of SEQ ID NO: 1 coding for leghemoglobin and at least one sequence of SEQ ID NOS: 3 and/or 5 coding for hemoglobin.
34. (Previously presented) The method according to claim 28, characterized in that the plants are transformed in such a way that they comprise sequences with approximately 70% identity with one of the sequences of SEQ ID NOS: 1, 3 and/or 5.
35. (Previously presented) The method according to claim 28, characterized in that the plants are transformed in such a way that they produce starch and/or oil.
36. (Previously presented) The method according to claim 28, characterized in that monocotyledonous crop plants, in particular of the species Gramineae, are transformed.

37. (Previously presented) The method according to claim 28, characterized in that dicotyledonous crop plants, in particular from the family Asteraceae, Brassicaceae, Compositae, Cruciferae, Cucurbitaceae, Leguminosae, Rubiaceae, Solanaceae, Sterculiaceae, Theaceae, or Umbelliferae are transformed.
38. (Previously presented) The method according to claim 28, characterized in that potatoes, *Arabidopsis thaliana*, soybean or oilseed rape are transformed.
39. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one nucleotide sequence according to claim 15 is used for the transformation.
40. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one gene structure according to claim 16 is used for the transformation.
41. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one vector according to claim 17 is used for the transformation.
42. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one nucleotide sequence according to claim 20 is used for the transformation.
43. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one gene structure according to claim 21 is used for the transformation.
44. (Previously presented) A method for modifying the storage reserve content in plants, characterized in that at least one vector according to claim 22 is used for the transformation.
45. (Previously presented) A method for the production of starch and/or oil, characterized in that a plant according to claim 4 is used and the starch and/or oil is recovered.